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Sequence Listing

<110> Botstein,David
Desnoyers,Luc
Ferrara,Napoleone
Fong,Sherman
Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
Tumas,Daniel
Watanabe,Colin K.
Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
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Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
50 55 60
Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
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 35 40 45
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 His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu
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 Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu
 80 85 90
 Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly
 95 100 105

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Val	Gly	Glu	Ala	Gly	Leu	Pro	Trp	Asn	Phe	Gly	Pro	Leu	Ser	Lys	800	805	810
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<213> Homo sapiens

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50 55 60
Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
65 70 75
Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
80 85 90
Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
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<210> 10
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Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
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Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
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 Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
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 Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
 65 70 75
 Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
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 Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
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Pro Ala Leu Phe	Ser Arg Glu Asn Tyr	Gly Arg Leu Arg Leu	Ile		
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Thr Ser Ser Lys	His Arg Cys Met Asp	Ser Ser Ala Ala Phe	Leu		
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Ile Asn Ser Arg	Ser Ser Cys Thr Leu	Phe Gln Asp Ile Phe	Gln		
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Ser Ser Pro Val	Ile Leu Gln Phe Gly	His Ala Glu Thr Leu	Leu		
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Pro Leu Leu Ser	Leu Met Gly Tyr Phe	Lys Asp Lys Glu Pro	Leu		
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Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
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Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
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Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly	260	265	270	
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro	275	280	285	
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ccttgccctt ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700
 atggccccct acatgaaacg gctttcccgg ggccaaacgg tggaggatct 2750
 gctggagggt ctgagtgaca tagacgagat gtcccggcgg agacccgaga 2800
 tccctgagctt cttctcgacc aacctgcagc ggctgatgag ctcggccgag 2850
 gagtgttgcc gcaacctcgc cttcagcctg gccctgcgct ccatgcagaa 2900
 cagccccagc attgcagccg ctttctctgcc cacgttcatg tactgcctgg 2950
 gcagccagga ctttgagggt gtgcagacgg cctccggaa cctgcctgag 3000
 tacgtctctc tgtgccaaga gcacgcggct gtgctgctcc accgggcctt 3050
 cctggtgggc atgtacggcc agatggaccc cagcgcgcag atctccgagg 3100
 ccctgaggat cctgcatatg gaggccgtga tgtgagcctg tggcagccga 3150
 cccccctcca agccccggcc cgtcccgtcc ccggggatcc tcgaggcaaa 3200
 gcccaggaag cgtgggcgtt gctggtctgt ccgaggaggt gagggcgcg 3250
 agccctgagg ccaggcaggc ccaggagcaa tactccgagc cctgggggtgg 3300
 ctccgggccc gccgctggca tcaggggccc tccagcaagc cctcattcac 3350
 cttctggggc acagccctgc cgcggagcgg cggatcccc cgggcatggc 3400
 ctgggctggt tttgaatgaa acgacctgaa ctgtcaa 3437

<210> 22
 <211> 1029
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met His Ile Leu Val Val His Ala Met Val Ile Leu Leu Thr Leu
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 Gly Pro Pro Arg Ala Asp Asp Ser Glu Phe Gln Ala Leu Leu Asp
 20 25 30
 Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
 35 40 45
 Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
 50 55 60
 Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
 65 70 75
 Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
 80 85 90
 Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
 95 100 105

Gln	Ala	Val	Ala	His	Asp	Pro	Gln	Thr	Leu	Glu	Gln	Asn	Ile	Met	110	115	120
Asp	Lys	Asn	Tyr	Met	Ala	His	Leu	Val	Glu	Val	Gln	His	Glu	Arg	125	130	135
Gly	Ala	Ser	Gly	Gly	Gln	Thr	Phe	His	Ser	Leu	Leu	Thr	Ala	Ser	140	145	150
Leu	Pro	Pro	Arg	Arg	Asp	Ser	Thr	Glu	Ala	Pro	Lys	Pro	Lys	Ser	155	160	165
Ser	Pro	Glu	Gln	Pro	Ile	Gly	Gln	Gly	Arg	Ile	Arg	Val	Gly	Thr	170	175	180
Gln	Leu	Arg	Val	Leu	Gly	Pro	Glu	Asp	Asp	Leu	Ala	Gly	Met	Phe	185	190	195
Leu	Gln	Ile	Phe	Pro	Leu	Ser	Pro	Asp	Pro	Arg	Trp	Gln	Ser	Ser	200	205	210
Ser	Pro	Arg	Pro	Val	Ala	Leu	Ala	Leu	Gln	Gln	Ala	Leu	Gly	Gln	215	220	225
Glu	Leu	Ala	Arg	Val	Val	Gln	Gly	Ser	Pro	Glu	Val	Pro	Gly	Ile	230	235	240
Thr	Val	Arg	Val	Leu	Gln	Ala	Leu	Ala	Thr	Leu	Leu	Ser	Ser	Pro	245	250	255
His	Gly	Gly	Ala	Leu	Val	Met	Ser	Met	His	Arg	Ser	His	Phe	Leu	260	265	270
Ala	Cys	Pro	Leu	Leu	Arg	Gln	Leu	Cys	Gln	Tyr	Gln	Arg	Cys	Val	275	280	285
Pro	Gln	Asp	Thr	Gly	Phe	Ser	Ser	Leu	Phe	Leu	Lys	Val	Leu	Leu	290	295	300
Gln	Met	Leu	Gln	Trp	Leu	Asp	Ser	Pro	Gly	Val	Glu	Gly	Gly	Pro	305	310	315
Leu	Arg	Ala	Gln	Leu	Arg	Met	Leu	Ala	Ser	Gln	Ala	Ser	Ala	Gly	320	325	330
Arg	Arg	Leu	Ser	Asp	Val	Arg	Gly	Gly	Leu	Leu	Arg	Leu	Ala	Glu	335	340	345
Ala	Leu	Ala	Phe	Arg	Gln	Asp	Leu	Glu	Val	Val	Ser	Ser	Thr	Val	350	355	360
Arg	Ala	Val	Ile	Ala	Thr	Leu	Arg	Ser	Gly	Glu	Gln	Cys	Ser	Val	365	370	375
Glu	Pro	Asp	Leu	Ile	Ser	Lys	Val	Leu	Gln	Gly	Leu	Ile	Glu	Val	380	385	390
Arg	Ser	Pro	His	Leu	Glu	Glu	Leu	Leu	Thr	Ala	Phe	Phe	Ser	Ala			

	395	400	405
Thr Ala Asp Ala	Ala Ser Pro Phe Pro	Ala Cys Lys Pro Val	Val
	410	415	420
Val Val Ser Ser	Leu Leu Leu Gln Glu	Glu Glu Pro Leu Ala	Gly
	425	430	435
Gly Lys Pro Gly	Ala Asp Gly Gly Ser	Leu Glu Ala Val Arg	Leu
	440	445	450
Gly Pro Ser Ser	Gly Leu Leu Val Asp	Trp Leu Glu Met Leu	Asp
	455	460	465
Pro Glu Val Val	Ser Ser Cys Pro Asp	Leu Gln Leu Arg Leu	Leu
	470	475	480
Phe Ser Arg Arg	Lys Gly Lys Gly Gln	Ala Gln Val Pro Ser	Phe
	485	490	495
Arg Pro Tyr Leu	Leu Thr Leu Phe Thr	His Gln Ser Ser Trp	Pro
	500	505	510
Thr Leu His Gln	Cys Ile Arg Val Leu	Leu Gly Lys Ser Arg	Glu
	515	520	525
Gln Arg Phe Asp	Pro Ser Ala Ser Leu	Asp Phe Leu Trp Ala	Cys
	530	535	540
Ile His Val Pro	Arg Ile Trp Gln Gly	Arg Asp Gln Arg Thr	Pro
	545	550	555
Gln Lys Arg Arg	Glu Glu Leu Val Leu	Arg Val Gln Gly Pro	Glu
	560	565	570
Leu Ile Ser Leu	Val Glu Leu Ile Leu	Ala Glu Ala Glu Thr	Arg
	575	580	585
Ser Gln Asp Gly	Asp Thr Ala Ala Cys	Ser Leu Ile Gln Ala	Arg
	590	595	600
Leu Pro Leu Leu	Leu Ser Cys Cys Cys	Gly Asp Asp Glu Ser	Val
	605	610	615
Arg Lys Val Thr	Glu His Leu Ser Gly	Cys Ile Gln Gln Trp	Gly
	620	625	630
Asp Ser Val Leu	Gly Arg Arg Cys Arg	Asp Leu Leu Leu Gln	Leu
	635	640	645
Tyr Leu Gln Arg	Pro Glu Leu Arg Val	Pro Val Pro Glu Val	Leu
	650	655	660
Leu His Ser Glu	Gly Ala Ala Ser Ser	Ser Val Cys Lys Leu	Asp
	665	670	675
Gly Leu Ile His	Arg Phe Ile Thr Leu	Leu Ala Asp Thr Ser	Asp
	680	685	690

Ser	Arg	Ala	Leu	Glu	Asn	Arg	Gly	Ala	Asp	Ala	Ser	Met	Ala	Cys	695	700	705
Arg	Lys	Leu	Ala	Val	Ala	His	Pro	Leu	Leu	Leu	Arg	His	Leu		710	715	720
Pro	Met	Ile	Ala	Ala	Leu	Leu	His	Gly	Arg	Thr	His	Leu	Asn	Phe	725	730	735
Gln	Glu	Phe	Arg	Gln	Gln	Asn	His	Leu	Ser	Cys	Phe	Leu	His	Val	740	745	750
Leu	Gly	Leu	Leu	Glu	Leu	Leu	Gln	Pro	His	Val	Phe	Arg	Ser	Glu	755	760	765
His	Gln	Gly	Ala	Leu	Trp	Asp	Cys	Leu	Leu	Ser	Phe	Ile	Arg	Leu	770	775	780
Leu	Leu	Asn	Tyr	Arg	Lys	Ser	Ser	Arg	His	Leu	Ala	Ala	Phe	Ile	785	790	795
Asn	Lys	Phe	Val	Gln	Phe	Ile	His	Lys	Tyr	Ile	Thr	Tyr	Asn	Ala	800	805	810
Pro	Ala	Ala	Ile	Ser	Phe	Leu	Gln	Lys	His	Ala	Asp	Pro	Leu	His	815	820	825
Asp	Leu	Ser	Phe	Asp	Asn	Ser	Asp	Leu	Val	Met	Leu	Lys	Ser	Leu	830	835	840
Leu	Ala	Gly	Leu	Ser	Leu	Pro	Ser	Arg	Asp	Asp	Arg	Thr	Asp	Arg	845	850	855
Gly	Leu	Asp	Glu	Glu	Gly	Glu	Glu	Glu	Ser	Ser	Ala	Gly	Ser	Leu	860	865	870
Pro	Leu	Val	Ser	Val	Ser	Leu	Phe	Thr	Pro	Leu	Thr	Ala	Ala	Glu	875	880	885
Met	Ala	Pro	Tyr	Met	Lys	Arg	Leu	Ser	Arg	Gly	Gln	Thr	Val	Glu	890	895	900
Asp	Leu	Leu	Glu	Val	Leu	Ser	Asp	Ile	Asp	Glu	Met	Ser	Arg	Arg	905	910	915
Arg	Pro	Glu	Ile	Leu	Ser	Phe	Phe	Ser	Thr	Asn	Leu	Gln	Arg	Leu	920	925	930
Met	Ser	Ser	Ala	Glu	Glu	Cys	Cys	Arg	Asn	Leu	Ala	Phe	Ser	Leu	935	940	945
Ala	Leu	Arg	Ser	Met	Gln	Asn	Ser	Pro	Ser	Ile	Ala	Ala	Ala	Phe	950	955	960
Leu	Pro	Thr	Phe	Met	Tyr	Cys	Leu	Gly	Ser	Gln	Asp	Phe	Glu	Val	965	970	975
Val	Gln	Thr	Ala	Leu	Arg	Asn	Leu	Pro	Glu	Tyr	Ala	Leu	Leu	Cys			

980	985	990
Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly		
995	1000	1005
Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu		
1010	1015	1020
Arg Ile Leu His Met Glu Ala Val Met		
1025		

<210> 23
 <211> 2186
 <212> DNA
 <213> Homo sapiens

<400> 23
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 atgaggctcc gcaatggcac ctctctgacg ctgctgctct tctgcctgtg 100
 cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150
 acgttggtga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200
 cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250
 gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300
 gagacggcaa tcgcacctgg gccgcctaa cagaggaccc ccgattgaag 350
 ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400
 tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450
 gcgtgggcca gggccgcacc ggagtgtcgg tggatgatgg catcccagac 500
 gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550
 ctccgagctg agcccgcagg agaaggagga ctcggtcatc gtggtgctga 600
 tcgccgagac tgactcacag tacacttcgg cagtgcaga gaacatcaag 650
 gccttggtcc ccacggagat ccattctggg ctcttgagg tcattctacc 700
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 ttctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850
 ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900
 cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950
 ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000
 gttcattctc atgttctacc gggacaagcc catcgactgg ctctgggacc 1050

atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100
 gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150
 gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200
 acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250
 gcagaggtga gcacgagcct gaagacatac cagcacttca ccctggagaa 1300
 agcctacctg cgcgaggact tcttctgggc cttcaccctt gccgcggggg 1350
 acttcatccg ctccgcttc ttccaacctc taagactgga gcggttcttc 1400
 ttccgcagtg ggaacatcga gcacccggag gacaagctct tcaacacgtc 1450
 tgtggagggtg ctgcccttcg acaaccctca gtcagacaag gaggccctgc 1500
 aggagggccg caccgccacc ctccggtacc ctccggagccc cgacggctac 1550
 ctccagatcg gctccttcta caagggagtg gcagagggag aggtggaccc 1600
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 ggaggcccta ggagctgggtg ctgccccgc ccgccggggc gcggaggagg 1900
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 tgccccagtc aggcggtttt agaagagctt ttacttgggc gccgcgcgtc 2000
 tctggcgcga acactggaat gcatatacta ctttatgtgc tgtgtttttt 2050
 attcttgat acatttgatt ttttcacgta agtccacata tacttctata 2100
 agagcgtgac ttgtaataaa ggggttaatga agaaaaaaaa aaaaaaaaaa 2150
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186

<210> 24
 <211> 548
 <212> PRT
 <213> Homo sapiens

<400> 24
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 1 5 10 15
 Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly
 20 25 30

Gln	Lys	Gly	Asp	Val	Val	Asp	Val	Tyr	Gln	Arg	Glu	Phe	Leu	Ala		35	40	45
Leu	Arg	Asp	Arg	Leu	His	Ala	Ala	Glu	Gln	Glu	Ser	Leu	Lys	Arg		50	55	60
Ser	Lys	Glu	Leu	Asn	Leu	Val	Leu	Asp	Glu	Ile	Lys	Arg	Ala	Val		65	70	75
Ser	Glu	Arg	Gln	Ala	Leu	Arg	Asp	Gly	Asp	Gly	Asn	Arg	Thr	Trp		80	85	90
Gly	Arg	Leu	Thr	Glu	Asp	Pro	Arg	Leu	Lys	Pro	Trp	Asn	Gly	Ser		95	100	105
His	Arg	His	Val	Leu	His	Leu	Pro	Thr	Val	Phe	His	His	Leu	Pro		110	115	120
His	Leu	Leu	Ala	Lys	Glu	Ser	Ser	Leu	Gln	Pro	Ala	Val	Arg	Val		125	130	135
Gly	Gln	Gly	Arg	Thr	Gly	Val	Ser	Val	Val	Met	Gly	Ile	Pro	Ser		140	145	150
Val	Arg	Arg	Glu	Val	His	Ser	Tyr	Leu	Thr	Asp	Thr	Leu	His	Ser		155	160	165
Leu	Ile	Ser	Glu	Leu	Ser	Pro	Gln	Glu	Lys	Glu	Asp	Ser	Val	Ile		170	175	180
Val	Val	Leu	Ile	Ala	Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Ala	Val		185	190	195
Thr	Glu	Asn	Ile	Lys	Ala	Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	Gly		200	205	210
Leu	Leu	Glu	Val	Ile	Ser	Pro	Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe		215	220	225
Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly	Asp	Pro	Lys	Glu	Arg	Val	Arg		230	235	240
Trp	Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr	Cys	Phe	Leu	Met	Met	Tyr		245	250	255
Ala	Gln	Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln	Leu	Glu	Asp	Asp	Ile		260	265	270
Val	Ala	Lys	Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys	Asn	Phe	Ala	Leu		275	280	285
Gln	Gln	Pro	Ser	Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe	Ser	Gln	Leu		290	295	300
Gly	Phe	Ile	Gly	Lys	Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser	Leu	Ile		305	310	315
Val	Glu	Phe	Ile	Leu	Met	Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp	Trp				

320	325	330
Leu Leu Asp His Ile Leu Trp Val Lys	Val Cys Asn Pro Glu Lys	
335	340	345
Asp Ala Lys His Cys Asp Arg Gln Lys	Ala Asn Leu Arg Ile Arg	
350	355	360
Phe Lys Pro Ser Leu Phe Gln His Val	Gly Thr His Ser Ser Leu	
365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp	Lys Asp Phe Gly Lys Gln	
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro	Pro Ala Glu Val Ser Thr	
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr	Leu Glu Lys Ala Tyr Leu	
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr	Pro Ala Ala Gly Asp Phe	
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu	Arg Leu Glu Arg Phe Phe	
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro	Glu Asp Lys Leu Phe Asn	
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp	Asn Pro Gln Ser Asp Lys	
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala	Thr Leu Arg Tyr Pro Arg	
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly	Ser Phe Tyr Lys Gly Val	
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe	Gly Pro Leu Glu Ala Leu	
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro	Val Trp Val Ile Leu Ser	
530	535	540
Glu Ile Phe Leu Lys Lys Ala Asp		
545		

<210> 25

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 25

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 26
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 27
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

<400> 27
 actcgggatt cctgctgtt 19

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

<400> 28
 aggcctttac ccaaggccac aac 23

<210> 29
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

<400> 29
 ggccctgtcct gtgtttctca 19

<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

<400> 30
 tcccaccact tacttccatg aa 22

<210> 31
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 31

ctgtggtacc caattgccgc cttgt 25

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 32

attgtcctga gattcgagca aga 23

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 33

gtccagcaag ccctcatt 18

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 34

cttctgggcc acagccctgc 20

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 35

cagttcaggt cgtttcattc a 21

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 36

ccagtcaggc cgtttttaga 19

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 37

cgggcgccca agtaaaagct c 21

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 38

cataaagtag tatatgcatt ccagtgtt 28